

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(i) APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene

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(ii) TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

(iii) NUMBER OF SEQUENCES: 19

15

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Immunex Corporation, Law Department
(B) STREET: 51 University Street
(C) CITY: Seattle
(D) STATE: WA
(E) COUNTRY: USA
(F) ZIP: 98101

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: Apple Power Macintosh
(C) OPERATING SYSTEM: Apple Operating System 7.5.5
(D) SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

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(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 22 DECEMBER 1997
(C) CLASSIFICATION:

30

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: USSN 60/064,671
(B) FILING DATE: 14 OCTOBER 1997
(C) CLASSIFICATION:

35

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: USSN 08/813,509
(B) FILING DATE: 07 MARCH 1997
(C) CLASSIFICATION:

40

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: USSN 08/772,330 (60/064,671)
(B) FILING DATE: 23 DECEMBER 1996
(C) CLASSIFICATION:

45

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Perkins, Patricia Anne
(B) REGISTRATION NUMBER: 34,693
(C) REFERENCE/DOCKET NUMBER: 2852-A

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(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (206)587-0430
(B) TELEFAX: (206)233-0644

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(2) INFORMATION FOR SEQ ID NO:1:

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(i) SEQUENCE CHARACTERISTICS:

IMMUNEX CORPORATION

Docket No. 2852-A

(A) LENGTH: 3115 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

10

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: HOMO SAPIENS

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(vii) IMMEDIATE SOURCE:

(A) LIBRARY: BONE-MARROW DERIVED DENDRITIC CELLS

(B) CLONE: 9D-8A

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(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 93..1868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

25

GCTGCTGCTG CTCTGCGCGC TGCTCGCCCG GCTGCAGTTT TATCCAGAAA GAGCTGTGTG 60

GACTCTCTGC CTGACCTCAG TGTTCTTTTC AG GTG GCT TTG CAG ATC GCT CCT 113

30

Val Ala Leu Gln Ile Ala Pro
1 5

CCA TGT ACC AGT GAG AAG CAT TAT GAG CAT CTG GGA CGG TGC TGT AAC 161

Pro Cys Thr Ser Glu Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn
10 15 20

35

AAA TGT GAA CCA GGA AAG TAC ATG TCT TCT AAA TGC ACT ACT ACC TCT 209

Lys Cys Glu Pro Gly Lys Tyr Met Ser Ser Lys Cys Thr Thr Thr Ser
25 30 35

40

GAC AGT GTA TGT CTG CCC TGT GGC CCG GAT GAA TAC TTG GAT AGC TGG 257

Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp
40 45 50 55

45

AAT GAA GAA GAT AAA TGC TTG CTG CAT AAA GTT TGT GAT ACA GGC AAG 305

Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys
60 65 70

50

GCC CTG GTG GCC GTG GTC GCC GGC AAC AGC ACG ACC CCC CGG CGC TGC 353

Ala Leu Val Ala Val Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys
75 80 85

55

GCG TGC ACG GCT GGG TAC CAC TGG AGC CAG GAC TGC GAG TGC TGC CGC 401

Ala Cys Thr Ala Gly Tyr His Trp Ser Gln Asp Cys Glu Cys Cys Arg
90 95 100

CGC AAC ACC GAG TGC GCG CCG GGC CTG GGC GCC CAG CAC CCG TTG CAG 449

Arg Asn Thr Glu Cys Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln
105 110 115

IMMUNEX CORPORATION

Docket No. 2852-A

	CTC	AAC	AAG	GAC	ACA	GTG	TGC	AAA	CCT	TGC	CTT	GCA	GGC	TAC	TTC	TCT	497
	Leu	Asn	Lys	Asp	Thr	Val	Cys	Lys	Pro	Cys	Leu	Ala	Gly	Tyr	Phe	Ser	
	120					125					130					135	
5	GAT	GCC	TTT	TCC	TCC	ACG	GAC	AAA	TGC	AGA	CCC	TGG	ACC	AAC	TGT	ACC	545
	Asp	Ala	Phe	Ser	Ser	Thr	Asp	Lys	Cys	Arg	Pro	Trp	Thr	Asn	Cys	Thr	
					140					145					150		
10	TTC	CTT	GGA	AAG	AGA	GTA	GAA	CAT	CAT	GGG	ACA	GAG	AAA	TCC	GAT	GCG	593
	Phe	Leu	Gly	Lys	Arg	Val	Glu	His	His	Gly	Thr	Glu	Lys	Ser	Asp	Ala	
				155				160						165			
15	GTT	TGC	AGT	TCT	TCT	CTG	CCA	GCT	AGA	AAA	CCA	CCA	AAT	GAA	CCC	CAT	641
	Val	Cys	Ser	Ser	Ser	Leu	Pro	Ala	Arg	Lys	Pro	Pro	Asn	Glu	Pro	His	
			170					175					180				
20	GTT	TAC	TTG	CCC	GGT	TTA	ATA	ATT	CTG	CTT	CTC	TTC	GCG	TCT	GTG	GCC	689
	Val	Tyr	Leu	Pro	Gly	Leu	Ile	Ile	Leu	Leu	Leu	Phe	Ala	Ser	Val	Ala	
			185				190					195					
25	CTG	GTG	GCT	GCC	ATC	ATC	TTT	GGC	GTT	TGC	TAT	AGG	AAA	AAA	GGG	AAA	737
	Leu	Val	Ala	Ala	Ile	Ile	Phe	Gly	Val	Cys	Tyr	Arg	Lys	Lys	Gly	Lys	
	200				205						210				215		
30	GCA	CTC	ACA	GCT	AAT	TTG	TGG	CAC	TGG	ATC	AAT	GAG	GCT	TGT	GGC	CGC	785
	Ala	Leu	Thr	Ala	Asn	Leu	Trp	His	Trp	Ile	Asn	Glu	Ala	Cys	Gly	Arg	
				220					225					230			
35	CTA	AGT	GGA	GAT	AAG	GAG	TCC	TCA	GGT	GAC	AGT	TGT	GTC	AGT	ACA	CAC	833
	Leu	Ser	Gly	Asp	Lys	Glu	Ser	Ser	Gly	Asp	Ser	Cys	Val	Ser	Thr	His	
				235				240						245			
40	ACG	GCA	AAC	TTT	GGT	CAG	CAG	GGA	GCA	TGT	GAA	GGT	GTC	TTA	CTG	CTG	881
	Thr	Ala	Asn	Phe	Gly	Gln	Gln	Gly	Ala	Cys	Glu	Gly	Val	Leu	Leu	Leu	
			250					255					260				
45	ACT	CTG	GAG	GAG	AAG	ACA	TTT	CCA	GAA	GAT	ATG	TGC	TAC	CCA	GAT	CAA	929
	Thr	Leu	Glu	Glu	Lys	Thr	Phe	Pro	Glu	Asp	Met	Cys	Tyr	Pro	Asp	Gln	
		265					270					275					
50	GGT	GGT	GTC	TGT	CAG	GGC	ACG	TGT	GTA	GGA	GGT	GGT	CCC	TAC	GCA	CAA	977
	Gly	Gly	Val	Cys	Gln	Gly	Thr	Cys	Val	Gly	Gly	Gly	Pro	Tyr	Ala	Gln	
	280				285						290				295		
55	GGC	GAA	GAT	GCC	AGG	ATG	CTC	TCA	TTG	GTC	AGC	AAG	ACC	GAG	ATA	GAG	1025
	Gly	Glu	Asp	Ala	Arg	Met	Leu	Ser	Leu	Val	Ser	Lys	Thr	Glu	Ile	Glu	
				300					305					310			
60	GAA	GAC	AGC	TTC	AGA	CAG	ATG	CCC	ACA	GAA	GAT	GAA	TAC	ATG	GAC	AGG	1073
	Glu	Asp	Ser	Phe	Arg	Gln	Met	Pro	Thr	Glu	Asp	Glu	Tyr	Met	Asp	Arg	
				315				320					325				
65	CCC	TCC	CAG	CCC	ACA	GAC	CAG	TTA	CTG	TTC	CTC	ACT	GAG	CCT	GGA	AGC	1121
	Pro	Ser	Gln	Pro	Thr	Asp	Gln	Leu	Leu	Phe	Leu	Thr	Glu	Pro	Gly	Ser	
			330					335					340				
70	AAA	TCC	ACA	CCT	CCT	TTC	TCT	GAA	CCC	CTG	GAG	GTG	GGG	GAG	AAT	GAC	1169
	Lys	Ser	Thr	Pro	Pro	Phe	Ser	Glu	Pro	Leu	Glu	Val	Gly	Glu	Asn	Asp	
			345				350					355					

IMMUNEX CORPORATION

Docket No. 2852-A

	AGT	TTA	AGC	CAG	TGC	TTC	ACG	GGG	ACA	CAG	AGC	ACA	GTG	GGT	TCA	GAA	1217
	Ser	Leu	Ser	Gln	Cys	Phe	Thr	Gly	Thr	Gln	Ser	Thr	Val	Gly	Ser	Glu	
	360					365					370					375	
5	AGC	TGC	AAC	TGC	ACT	GAG	CCC	CTG	TGC	AGG	ACT	GAT	TGG	ACT	CCC	ATG	1265
	Ser	Cys	Asn	Cys	Thr	Glu	Pro	Leu	Cys	Arg	Thr	Asp	Trp	Thr	Pro	Met	
					380					385					390		
10	TCC	TCT	GAA	AAC	TAC	TTG	CAA	AAA	GAG	GTG	GAC	AGT	GGC	CAT	TGC	CCG	1313
	Ser	Ser	Glu	Asn	Tyr	Leu	Gln	Lys	Glu	Val	Asp	Ser	Gly	His	Cys	Pro	
					395				400					405			
15	CAC	TGG	GCA	GCC	AGC	CCC	AGC	CCC	AAC	TGG	GCA	GAT	GTG	TGC	ACA	GGC	1361
	His	Trp	Ala	Ala	Ser	Pro	Ser	Pro	Asn	Trp	Ala	Asp	Val	Cys	Thr	Gly	
			410					415					420				
20	TGC	CGG	AAC	CCT	CCT	GGG	GAG	GAC	TGT	GAA	CCC	CTC	GTG	GGT	TCC	CCA	1409
	Cys	Arg	Asn	Pro	Pro	Gly	Glu	Asp	Cys	Glu	Pro	Leu	Val	Gly	Ser	Pro	
		425				430						435					
25	AAA	CGT	GGA	CCC	TTG	CCC	CAG	TGC	GCC	TAT	GGC	ATG	GGC	CTT	CCC	CCT	1457
	Lys	Arg	Gly	Pro	Leu	Pro	Gln	Cys	Ala	Tyr	Gly	Met	Gly	Leu	Pro	Pro	
		440				445					450				455		
30	GAA	GAA	GAA	GCC	AGC	AGG	ACG	GAG	GCC	AGA	GAC	CAG	CCC	GAG	GAT	GGG	1505
	Glu	Glu	Glu	Ala	Ser	Arg	Thr	Glu	Ala	Arg	Asp	Gln	Pro	Glu	Asp	Gly	
					460					465					470		
35	GCT	GAT	GGG	AGG	CTC	CCA	AGC	TCA	GCG	AGG	GCA	GGT	GCC	GGG	TCT	GGA	1553
	Ala	Asp	Gly	Arg	Leu	Pro	Ser	Ser	Ala	Arg	Ala	Gly	Ala	Gly	Ser	Gly	
				475					480					485			
40	AGC	TCC	CCT	GGT	GGC	CAG	TCC	CCT	GCA	TCT	GGA	AAT	GTG	ACT	GGA	AAC	1601
	Ser	Ser	Pro	Gly	Gly	Gln	Ser	Pro	Ala	Ser	Gly	Asn	Val	Thr	Gly	Asn	
			490					495					500				
45	AGT	AAC	TCC	ACG	TTC	ATC	TCC	AGC	GGG	CAG	GTG	ATG	AAC	TTC	AAG	GGC	1649
	Ser	Asn	Ser	Thr	Phe	Ile	Ser	Ser	Gly	Gln	Val	Met	Asn	Phe	Lys	Gly	
		505				510						515					
50	GAC	ATC	ATC	GTG	GTC	TAC	GTC	AGC	CAG	ACC	TCG	CAG	GAG	GGC	GCG	GCG	1697
	Asp	Ile	Ile	Val	Val	Tyr	Val	Ser	Gln	Thr	Ser	Gln	Glu	Gly	Ala	Ala	
		520				525					530				535		
55	GCG	GCT	GCG	GAG	CCC	ATG	GGC	CGC	CCG	GTG	CAG	GAG	GAG	ACC	CTG	GCG	1745
	Ala	Ala	Ala	Glu	Pro	Met	Gly	Arg	Pro	Val	Gln	Glu	Glu	Thr	Leu	Ala	
					540				545					550			
60	CGC	CGA	GAC	TCC	TTC	GCG	GGG	AAC	GGC	CCG	CGC	TTC	CCG	GAC	CCG	TGC	1793
	Arg	Arg	Asp	Ser	Phe	Ala	Gly	Asn	Gly	Pro	Arg	Phe	Pro	Asp	Pro	Cys	
				555					560					565			
65	GGC	GGC	CCC	GAG	GGG	CTG	CGG	GAG	CCG	GAG	AAG	GCC	TCG	AGG	CCG	GTG	1841
	Gly	Gly	Pro	Glu	Gly	Leu	Arg	Glu	Pro	Glu	Lys	Ala	Ser	Arg	Pro	Val	
			570					575					580				
70	CAG	GAG	CAA	GGC	GGG	GCC	AAG	GCT	TGA	GCGCCCCCA	TGGCTGGGAG						1888
	Gln	Glu	Gln	Gly	Gly	Ala	Lys	Ala									
			585				590										
75	CCCGAAGCTC	GGAGCCAGGG	CTCGCGAGGG	CAGCACCGCA	GCCTCTGCC	CAGCCCCGGC											1948

CACCCAGGGA TCGATCGTGA CAGTCGAGGA AGACCACCCG GCATTCTCTG CCCACTTTGC 2008
 CTTCACAGAA ATGGGCTTTT CAGGAAGTGA ATTGATGAGG ACTGTCCCA TGCCACCGGA 2068
 5 TGCTCAGCAG CCCGCCGCAC TGGGGCAGAT GTCTCCCTG CCACTCCTCA AACTCGCAGC 2128
 AGTAATTTGT GGCACATGGA CAGCTATTTT TATGACTATC CTGTTCTGTG GGGGGGGGT 2188
 10 CTATGTTTTT CCCCCATATT TGTATTCCTT TTCATAACTT TTCTTGATAT CTTTCCTCCC 2248
 TCTTTTTTAA TGTAAAGGTT TTCTCAAAAA TTCTCCTAAA GGTGAGGGTC TCTTTCTTTT 2308
 CTCTTTTCTT TTTTMTTTC TTTTMTTGGC AACCTGGCTC TGGCCACGGC TAGAGTGCAG 2368
 15 TGGTGCAGATT ATAGCCCGGT GCAGCCTCTA ACTCCTGGGC TCAAGCAATC CAAGTGATCC 2428
 TCCACCTCA ACCTTCGGAG TAGCTGGGAT CACAGCTGCA GGCCACGCCC AGCTTCCTCC 2488
 20 CCCCAGCTCC CCCCCCCCAG AGACACGGTC CCACCATGTT ACCCAGCCTG GTCTCAAACT 2548
 CCCCAGCTAA AGCAGTCTCT CAGCCTCGGC CTCCCAAAGT ACTGGGATTA CAGGCGTGAG 2608
 CCCCACCGCT GGCTGCTTT ACGTATTTTC TTTTGTGCC CTGCTCAGAG TGTTTTAGAG 2668
 25 ATGGCTTTCC CAGTGTGTGT TCATTGTAAA CACTTTTGGG AAAGGGCTAA ACATGTGAGG 2728
 CCTGGAGATA GTTGCTAAGT TGCTAGGAAC ATGTGGTGGG ACTTTCATAT TCTGAAAAAT 2788
 30 GTTCTATATT CTCATTTTTC TAAAGAAAG AAAAAGGAA ACCCGATTTA TTCTCCTGA 2848
 ATCTTTTTAA GTTGTGTGCG TTCTTAAGC AGAACTAAGC TCAGTATGTG ACCTTACCCG 2908
 CTAGGTGGTT AATTTATCCA TGCTGGCAGA GGCACTCAGG TACTTGGTAA GCAAATTCT 2968
 35 AAAACTCCAA GTTGCTGCAG CTTGGCATTCT TTCTTATCT AGAGTCTCT CTGGAAAGA 3028
 TGGAGAAAAT GAACAGGACA TGGGGCTCCT GGAAAGAAAG GGCCCGGGA GTTCAAGGAA 3088
 40 GAATAAAGTT GAAATTTTAA AAAAAA 3115

(2) INFORMATION FOR SEQ ID NO:2:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 591 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

55 Val Ala Leu Gln Ile Ala Pro Pro Cys Thr Ser Glu Lys His Tyr Glu
 1 5 10 15
 His Leu Gly Arg Cys Cys Asn Lys Cys Glu Pro Gly Lys Tyr Met Ser
 20 25 30
 60 Ser Lys Cys Thr Thr Thr Ser Asp Ser Val Cys Leu Pro Cys Gly Pro
 35 40 45

IMMUNEX CORPORATION

Docket No. 2852-A

Asp Glu Tyr Leu Asp Ser Trp Asn Glu Glu Asp Lys Cys Leu Leu His
 50 55 60

5 Lys Val Cys Asp Thr Gly Lys Ala Leu Val Ala Val Val Ala Gly Asn
 65 70 75 80

Ser Thr Thr Thr Pro Arg Cys Ala Cys Thr Ala Gly Tyr His Trp Ser
 85 90 95

10 Gln Asp Cys Glu Cys Cys Arg Arg Asn Thr Glu Cys Ala Pro Gly Leu
 100 105 110

15 Gly Ala Gln His Pro Leu Gln Leu Asn Lys Asp Thr Val Cys Lys Pro
 115 120 125

Cys Leu Ala Gly Tyr Phe Ser Asp Ala Phe Ser Ser Thr Asp Lys Cys
 130 135 140

20 Arg Pro Trp Thr Asn Cys Thr Phe Leu Gly Lys Arg Val Glu His His
 145 150 155 160

Gly Thr Glu Lys Ser Asp Ala Val Cys Ser Ser Ser Leu Pro Ala Arg
 165 170 175

25 Lys Pro Pro Asn Glu Pro His Val Tyr Leu Pro Gly Leu Ile Ile Leu
 180 185 190

30 Leu Leu Phe Ala Ser Val Ala Leu Val Ala Ala Ile Ile Phe Gly Val
 195 200 205

Cys Tyr Arg Lys Lys Gly Lys Ala Leu Thr Ala Asn Leu Trp His Trp
 210 215 220

35 Ile Asn Glu Ala Cys Gly Arg Leu Ser Gly Asp Lys Glu Ser Ser Gly
 225 230 235 240

Asp Ser Cys Val Ser Thr His Thr Ala Asn Phe Gly Gln Gln Gly Ala
 245 250 255

40 Cys Glu Gly Val Leu Leu Leu Thr Leu Glu Glu Lys Thr Phe Pro Glu
 260 265 270

45 Asp Met Cys Tyr Pro Asp Gln Gly Gly Val Cys Gln Gly Thr Cys Val
 275 280 285

Gly Gly Gly Pro Tyr Ala Gln Gly Glu Asp Ala Arg Met Leu Ser Leu
 290 295 300

50 Val Ser Lys Thr Glu Ile Glu Glu Asp Ser Phe Arg Gln Met Pro Thr
 305 310 315 320

Glu Asp Glu Tyr Met Asp Arg Pro Ser Gln Pro Thr Asp Gln Leu Leu
 325 330 335

55 Phe Leu Thr Glu Pro Gly Ser Lys Ser Thr Pro Pro Phe Ser Glu Pro
 340 345 350

60 Leu Glu Val Gly Glu Asn Asp Ser Leu Ser Gln Cys Phe Thr Gly Thr
 355 360 365

IMMUNEX CORPORATION

Docket No. 2852-A

Gln Ser Thr Val Gly Ser Glu Ser Cys Asn Cys Thr Glu Pro Leu Cys
 370 375 380

5 Arg Thr Asp Trp Thr Pro Met Ser Ser Glu Asn Tyr Leu Gln Lys Glu
 385 390 395 400

Val Asp Ser Gly His Cys Pro His Trp Ala Ala Ser Pro Ser Pro Asn
 405 410 415

10 Trp Ala Asp Val Cys Thr Gly Cys Arg Asn Pro Pro Gly Glu Asp Cys
 420 425 430

Glu Pro Leu Val Gly Ser Pro Lys Arg Gly Pro Leu Pro Gln Cys Ala
 435 440 445

15 Tyr Gly Met Gly Leu Pro Pro Glu Glu Glu Ala Ser Arg Thr Glu Ala
 450 455 460

20 Arg Asp Gln Pro Glu Asp Gly Ala Asp Gly Arg Leu Pro Ser Ser Ala
 465 470 475 480

Arg Ala Gly Ala Gly Ser Gly Ser Ser Pro Gly Gly Gln Ser Pro Ala
 485 490 495

25 Ser Gly Asn Val Thr Gly Asn Ser Asn Ser Thr Phe Ile Ser Ser Gly
 500 505 510

Gln Val Met Asn Phe Lys Gly Asp Ile Ile Val Val Tyr Val Ser Gln
 515 520 525

30 Thr Ser Gln Glu Gly Ala Ala Ala Ala Glu Pro Met Gly Arg Pro
 530 535 540

35 Val Gln Glu Glu Thr Leu Ala Arg Arg Asp Ser Phe Ala Gly Asn Gly
 545 550 555 560

Pro Arg Phe Pro Asp Pro Cys Gly Gly Pro Glu Gly Leu Arg Glu Pro
 565 570 575

40 Glu Lys Ala Ser Arg Pro Val Gln Glu Gln Gly Gly Ala Lys Ala
 580 585 590

(2) INFORMATION FOR SEQ ID NO:3:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1391 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 50 (ii) MOLECULE TYPE: cDNA
- 55 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: HOMO SAPIENS
- 60 (vii) IMMEDIATE SOURCE:

IMMUNEX CORPORATION

Docket No. 2852-A

(A) LIBRARY: BONE-MARROW DERIVED DENDRITIC CELLS
(B) CLONE: 9D-15C

(ix) FEATURE:

5 (A) NAME/KEY: CDS
(B) LOCATION: 39..1391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

10 CCGCTGAGGC CGCGCGCCCC GCCAGCCTGT CCCGCGCC ATG GCC CCG CGC GCC 53
Met Ala Pro Arg Ala
1 5

15 CGG CGG CGC CGC CCG CTG TTC GCG CTG CTG CTG CTC TGC GCG CTG CTC 101
Arg Arg Arg Arg Pro Leu Phe Ala Leu Leu Leu Leu Cys Ala Leu Leu
10 15 20

20 GCC CGG CTG CAG GTG GCT TTG CAG ATC GCT CCT CCA TGT ACC AGT GAG 149
Ala Arg Leu Gln Val Ala Leu Gln Ile Ala Pro Pro Cys Thr Ser Glu
25 30 35

25 AAG CAT TAT GAG CAT CTG GGA CGG TGC TGT AAC AAA TGT GAA CCA GGA 197
Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn Lys Cys Glu Pro Gly
40 45 50

30 AAG TAC ATG TCT TCT AAA TGC ACT ACT ACC TCT GAC AGT GTA TGT CTG 245
Lys Tyr Met Ser Ser Lys Cys Thr Thr Thr Ser Asp Ser Val Cys Leu
55 60 65

35 CCC TGT GGC CCG GAT GAA TAC TTG GAT AGC TGG AAT GAA GAA GAT AAA 293
Pro Cys Gly Pro Asp Tyr Leu Asp Ser Trp Asn Glu Glu Asp Lys
70 75 80 85

40 TGC TTG CTG CAT AAA GTT TGT GAT ACA GGC AAG GCC CTG GTG GCC GTG 341
Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys Ala Leu Val Ala Val
90 95 100

45 GTC GCC GGC AAC AGC ACG ACC CCC CGG CGC TGC GCG TGC ACG GCT GGG 389
Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys Ala Cys Thr Ala Gly
105 110 115

50 TAC CAC TGG AGC CAG GAC TGC GAG TGC TGC CGC CGC AAC ACC GAG TGC 437
Tyr His Trp Ser Gln Asp Cys Glu Cys Cys Arg Arg Asn Thr Glu Cys
120 125 130

55 GCG CCG GGC CTG GGC GCC CAG CAC CCG TTG CAG CTC AAC AAG GAC ACA 485
Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln Leu Asn Lys Asp Thr
135 140 145

60 GTG TGC AAA CCT TGC CTT GCA GGC TAC TTC TCT GAT GCC TTT TCC TCC 533
Val Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser Asp Ala Phe Ser Ser
150 155 160 165

55 ACG GAC AAA TGC AGA CCC TGG ACC AAC TGT ACC TTC CTT GGA AAG AGA 581
Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr Phe Leu Gly Lys Arg
170 175 180

60 GTA GAA CAT CAT GGG ACA GAG AAA TCC GAT GCG GTT TGC AGT TCT TCT 629
Val Glu His His Gly Thr Glu Lys Ser Asp Ala Val Cys Ser Ser Ser
185 190 195

IMMUNEX CORPORATION

Docket No. 2852-A

	CTG	CCA	GCT	AGA	AAA	CCA	CCA	AAT	GAA	CCC	CAT	GTT	TAC	TTG	CCC	GGT	677
	Leu	Pro	Ala	Arg	Lys	Pro	Pro	Asn	Glu	Pro	His	Val	Tyr	Leu	Pro	Gly	
			200					205					210				
5	TTA	ATA	ATT	CTG	CTT	CTC	TTC	GCG	TCT	GTG	GCC	CTG	GTG	GCT	GCC	ATC	725
	Leu	Ile	Ile	Leu	Leu	Leu	Phe	Ala	Ser	Val	Ala	Leu	Val	Ala	Ala	Ile	
		215					220					225					
10	ATC	TTT	GGC	GTT	TGC	TAT	AGG	AAA	AAA	GGG	AAA	GCA	CTC	ACA	GCT	AAT	773
	Ile	Phe	Gly	Val	Cys	Tyr	Arg	Lys	Lys	Gly	Lys	Ala	Leu	Thr	Ala	Asn	
		230				235						240				245	
15	TTG	TGG	CAC	TGG	ATC	AAT	GAG	GCT	TGT	GGC	CGC	CTA	AGT	GGA	GAT	AAG	821
	Leu	Trp	His	Trp	Ile	Asn	Glu	Ala	Cys	Gly	Arg	Leu	Ser	Gly	Asp	Lys	
					250					255					260		
	GAG	TCC	TCA	GGT	GAC	AGT	TGT	GTC	AGT	ACA	CAC	ACG	GCA	AAC	TTT	GGT	869
	Glu	Ser	Ser	Gly	Asp	Ser	Cys	Val	Ser	Thr	His	Thr	Ala	Asn	Phe	Gly	
				265					270					275			
20	CAG	CAG	GGA	GCA	TGT	GAA	GGT	GTC	TTA	CTG	CTG	ACT	CTG	GAG	GAG	AAG	917
	Gln	Gln	Gly	Ala	Cys	Glu	Gly	Val	Leu	Leu	Leu	Thr	Leu	Glu	Glu	Lys	
			280					285					290				
25	ACA	TTT	CCA	GAA	GAT	ATG	TGC	TAC	CCA	GAT	CAA	GGT	GGT	GTC	TGT	CAG	965
	Thr	Phe	Pro	Glu	Asp	Met	Cys	Tyr	Pro	Asp	Gln	Gly	Gly	Val	Cys	Gln	
		295					300					305					
30	GGC	ACG	TGT	GTA	GGA	GGT	GGT	CCC	TAC	GCA	CAA	GGC	GAA	GAT	GCC	AGG	1013
	Gly	Thr	Cys	Val	Gly	Gly	Gly	Pro	Tyr	Ala	Gln	Gly	Glu	Asp	Ala	Arg	
		310			315						320					325	
	ATG	CTC	TCA	TTG	GTC	AGC	AAG	ACC	GAG	ATA	GAG	GAA	GAC	AGC	TTC	AGA	1061
	Met	Leu	Ser	Leu	Val	Ser	Lys	Thr	Glu	Ile	Glu	Glu	Asp	Ser	Phe	Arg	
				330						335					340		
	CAG	ATG	CCC	ACA	GAA	GAT	GAA	TAC	ATG	GAC	AGG	CCC	TCC	CAG	CCC	ACA	1109
	Gln	Met	Pro	Thr	Glu	Asp	Glu	Tyr	Met	Asp	Arg	Pro	Ser	Gln	Pro	Thr	
				345					350					355			
	GAC	CAG	TTA	CTG	TTC	CTC	ACT	GAG	CCT	GGA	AGC	AAA	TCC	ACA	CCT	CCT	1157
	Asp	Gln	Leu	Leu	Phe	Leu	Thr	Glu	Pro	Gly	Ser	Lys	Ser	Thr	Pro	Pro	
			360					365					370				
45	TTC	TCT	GAA	CCC	CTG	GAG	GTG	GGG	GAG	AAT	GAC	AGT	TTA	AGC	CAG	TGC	1205
	Phe	Ser	Glu	Pro	Leu	Glu	Val	Gly	Glu	Asn	Asp	Ser	Leu	Ser	Gln	Cys	
			375				380					385					
50	TTC	ACG	GGG	ACA	CAG	AGC	ACA	GTG	GGT	TCA	GAA	AGC	TGC	AAC	TGC	ACT	1253
	Phe	Thr	Gly	Thr	Gln	Ser	Thr	Val	Gly	Ser	Glu	Ser	Cys	Asn	Cys	Thr	
			390			395					400				405		
	GAG	CCC	CTG	TGC	AGG	ACT	GAT	TGG	ACT	CCC	ATG	TCC	TCT	GAA	AAC	TAC	1301
	Glu	Pro	Leu	Cys	Arg	Thr	Asp	Trp	Thr	Pro	Met	Ser	Ser	Glu	Asn	Tyr	
				410						415					420		
	TTG	CAA	AAA	GAG	GTG	GAC	AGT	GGC	CAT	TGC	CCG	CAC	TGG	GCA	GCC	AGC	1349
	Leu	Gln	Lys	Glu	Val	Asp	Ser	Gly	His	Cys	Pro	His	Trp	Ala	Ala	Ser	
				425					430					435			
60																	

IMMUNEX CORPORATION

Docket No. 2852-A

CCC AGC CCC AAC TGG GCA GAT GTC TGC ACA GGC TGC CGG AAC
 Pro Ser Pro Asn Trp Ala Asp Val Cys Thr Gly Cys Arg Asn
 440 445 450

1391

5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 451 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Pro Arg Ala Arg Arg Arg Arg Pro Leu Phe Ala Leu Leu Leu
 1 5 10 15
 20 Leu Cys Ala Leu Leu Ala Arg Leu Gln Val Ala Leu Gln Ile Ala Pro
 20 25 30
 25 Pro Cys Thr Ser Glu Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn
 35 40 45
 30 Lys Cys Glu Pro Gly Lys Tyr Met Ser Ser Lys Cys Thr Thr Thr Ser
 50 55 60
 35 Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp
 65 70 75 80
 Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys
 85 90 95
 40 Ala Leu Val Ala Val Val Ala Gly Asn Ser Thr Thr Pro Arg Cys Cys
 100 105 110
 45 Ala Cys Thr Ala Gly Tyr His Trp Ser Gln Asp Cys Glu Cys Cys Arg
 115 120 125
 50 Arg Asn Thr Glu Cys Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln
 130 135 140
 55 Leu Asn Lys Asp Thr Val Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser
 145 150 155 160
 Asp Ala Phe Ser Ser Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr
 165 170 175
 60 Phe Leu Gly Lys Arg Val Glu His His Gly Thr Glu Lys Ser Asp Ala
 180 185 190
 Val Cys Ser Ser Ser Leu Pro Ala Arg Lys Pro Pro Asn Glu Pro His
 195 200 205
 Val Tyr Leu Pro Gly Leu Ile Ile Leu Leu Leu Phe Ala Ser Val Ala
 210 215 220
 Leu Val Ala Ala Ile Ile Phe Gly Val Cys Tyr Arg Lys Lys Gly Lys
 225 230 235 240

IMMUNEX CORPORATION

Docket No. 2852-A

Ala Leu Thr Ala Asn Leu Trp His Trp Ile Asn Glu Ala Cys Gly Arg
 245 250 255

5 Leu Ser Gly Asp Lys Glu Ser Ser Gly Asp Ser Cys Val Ser Thr His
 260 265 270

Thr Ala Asn Phe Gly Gln Gln Gly Ala Cys Glu Gly Val Leu Leu Leu
 275 280 285

10 Thr Leu Glu Glu Lys Thr Phe Pro Glu Asp Met Cys Tyr Pro Asp Gln
 290 295 300

15 Gly Gly Val Cys Gln Gly Thr Cys Val Gly Gly Gly Pro Tyr Ala Gln
 305 310 315 320

Gly Glu Asp Ala Arg Met Leu Ser Leu Val Ser Lys Thr Glu Ile Glu
 325 330 335

20 Glu Asp Ser Phe Arg Gln Met Pro Thr Glu Asp Glu Tyr Met Asp Arg
 340 345 350

Pro Ser Gln Pro Thr Asp Gln Leu Leu Phe Leu Thr Glu Pro Gly Ser
 355 360 365

25 Lys Ser Thr Pro Pro Phe Ser Glu Pro Leu Glu Val Gly Glu Asn Asp
 370 375 380

30 Ser Leu Ser Gln Cys Phe Thr Gly Thr Gln Ser Thr Val Gly Ser Glu
 385 390 395 400

Ser Cys Asn Cys Thr Glu Pro Leu Cys Arg Thr Asp Trp Thr Pro Met
 405 410 415

35 Ser Ser Glu Asn Tyr Leu Gln Lys Glu Val Asp Ser Gly His Cys Pro
 420 425 430

His Trp Ala Ala Ser Pro Ser Pro Asn Trp Ala Asp Val Cys Thr Gly
 435 440 445

40 Cys Arg Asn
 450

(2) INFORMATION FOR SEQ ID NO:5:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3136 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 50 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- 55 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: HOMO SAPIENS
- 60 (vii) IMMEDIATE SOURCE:

IMMUNEX CORPORATION

Docket No. 2852-A

(A) LIBRARY: BONE-MARROW DERIVED DENDRITIC CELLS
(B) CLONE: FULL LENGTH RANK

(ix) FEATURE:

5 (A) NAME/KEY: CDS
(B) LOCATION: 39..1886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

10 CCGCTGAGGC CGCGGCGCCC GCCAGCCTGT CCCGCGCC ATG GCC CCG CGC GCC 53
Met Ala Pro Arg Ala
1 5

15 CGG CGG CGC CGC CCG CTG TTC GCG CTG CTG CTG CTC TGC GCG CTG CTC 101
Arg Arg Arg Arg Pro Leu Phe Ala Leu Leu Leu Leu Cys Ala Leu Leu
10 15 20

20 GCC CGG CTG CAG GTG GCT TTG CAG ATC GCT CCT CCA TGT ACC AGT GAG 149
Ala Arg Leu Gln Val Ala Leu Gln Ile Ala Pro Pro Cys Thr Ser Glu
25 30 35

25 AAG CAT TAT GAG CAT CTG GGA CGG TGC TGT AAC AAA TGT GAA CCA GGA 197
Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn Lys Cys Glu Pro Gly
40 45 50

30 AAG TAC ATG TCT TCT AAA TGC ACT ACT ACC TCT GAC AGT GTA TGT CTG 245
Lys Tyr Met Ser Ser Lys Cys Thr Thr Thr Ser Ser Val Cys Leu
55 60 65

35 CCC TGT GGC CCG GAT GAA TAC TTG GAT AGC TGG AAT GAA GAA GAT AAA 293
Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp Asn Glu Glu Asp Lys
70 75 80 85

40 TGC TTG CTG CAT AAA GTT TGT GAT ACA GGC AAG GCC CTG GTG GCC GTG 341
Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys Ala Leu Val Ala Val
90 95 100

45 GTC GCC GGC AAC AGC ACG ACC CCC CGG CGC TGC GCG TGC ACG GCT GGG 389
Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys Ala Cys Thr Ala Gly
105 110 115

50 TAC CAC TGG AGC CAG GAC TGC GAG TGC TGC CGC CGC AAC ACC GAG TGC 437
Tyr His Trp Ser Gln Asp Cys Glu Cys Cys Arg Arg Asn Thr Glu Cys
120 125 130

55 GCG CCG GGC CTG GGC GCC CAG CAC CCG TTG CAG CTC AAC AAG GAC ACA 485
Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln Leu Asn Lys Asp Thr
135 140 145

60 GTG TGC AAA CCT TGC CTT GCA GGC TAC TTC TCT GAT GCC TTT TCC TCC 533
Val Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser Asp Ala Phe Ser Ser
150 155 160 165

55 ACG GAC AAA TGC AGA CCC TGG ACC AAC TGT ACC TTC CTT GGA AAG AGA 581
Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr Phe Leu Gly Lys Arg
170 175 180

60 GTA GAA CAT CAT GGG ACA GAG AAA TCC GAT GCG GTT TGC AGT TCT TCT 629
Val Glu His His Gly Thr Glu Lys Ser Asp Ala Val Cys Ser Ser Ser
185 190 195

IMMUNEX CORPORATION

Docket No. 2852-A

	CTG Leu	CCA Pro	GCT 200	AGA Arg	AAA Lys	CCA Pro	CCA Pro	AAT Asn	GAA Glu	CCC Pro	CAT His	GTT Val	TAC Tyr	TTG Leu	CCC Pro	GGT Gly	677
5	TTA Leu	ATA Ile	ATT Ile	CTG Leu	CTT Leu	CTC Leu	TTC 220	GCG Ala	TCT Ser	GTG Val	GCC Ala	CTG 225	GTG Val	GCT Ala	GCC Ala	ATC Ile	725
10	ATC Ile	TTT Phe	GGC Gly	GTT Val	TGC Cys	TAT Tyr	AGG 235	AAA Lys	AAA Lys	GGG Gly	AAA Lys	GCA 240	CTC Ala	ACA Leu	GCT Thr	AAT Ala	773
15	TTG Leu	TGG Trp	CAC His	TGG Trp	ATC Ile	AAT Asn	GAG Glu	GCT Ala	TGT Cys	GGC 255	CGC Arg	CTA Leu	AGT Ser	GGA Gly	GAT Asp	AAG Lys	821
20	GAG Glu	TCC Ser	TCA Ser	GGT Gly	GAC Asp	AGT Ser	TGT Cys	GTC Val	AGT 270	ACA Thr	CAC His	ACG Thr	GCA Ala	AAC Asn	TTT Phe	GGT Gly	869
	CAG Gln	CAG Gln	GGA 280	GCA Ala	TGT Cys	GAA Glu	GGT Gly	GTC 285	TTA Val	CTG Leu	CTG Leu	ACT Thr	CTG 290	GAG Leu	GAG Glu	AAG Lys	917
25	ACA Thr	TTT Phe	CCA Pro	GAA Glu	GAT Asp	ATG Met	TGC Cys	TAC 300	CCA Pro	GAT Asp	CAA Gln	GGT 305	GGT Gly	GTC Val	TGT Cys	CAG Gln	965
30	GGC Gly	ACG Thr	TGT Cys	GTA Val	GGA Gly	GGT Gly	GGT 315	CCC Gly	TAC Tyr	GCA Ala	CAA Gln	GGC 320	GAA Gly	GAT Glu	GCC Ala	AGG Arg	1013
35	ATG Met	CTC Leu	TCA Ser	TTG Leu	GTC Val	AGC Ser	AAG Lys	ACC Thr	GAG Glu	ATA Ile	GAG Glu	GAA Glu	GAC Asp	AGC Ser	TTC Phe	AGA Arg	1061
40	CAG Gln	ATG Met	CCC Pro	ACA Thr	GAA Glu	GAT Asp	GAA Glu	TAC Tyr	ATG 350	GAC Asp	AGG Arg	CCC Pro	TCC Ser	CAG Gln	CCC Pro	ACA Thr	1109
	GAC Asp	CAG Gln	TTA Leu	CTG Leu	TTC Phe	CTC Leu	ACT Thr	GAG 365	CCT Pro	GGA Gly	AGC Ser	AAA Lys	TCC 370	ACA Thr	CCT Pro	CCT Pro	1157
45	TTC Phe	TCT Ser	GAA Glu	CCC Pro	CTG Leu	GAG Glu	GTG Val	GGG 380	GAG Gly	AAT Asn	GAC Asp	AGT 385	TTA Ser	AGC Leu	CAG Gln	TGC Cys	1205
50	TTC Phe	ACG Thr	GGG Gly	ACA Thr	CAG Gln	AGC Ser	ACA Thr	GTG Val	GGT Gly	TCA Ser	GAA Glu	AGC 400	TGC Ser	AAC Cys	TGC Asn	ACT Thr	1253
55	GAG Glu	CCC Pro	CTG Leu	TGC Cys	AGG Arg	ACT Thr	GAT Asp	TGG Trp	ACT Thr	CCC 415	ATG Pro	TCC Met	TCT Ser	GAA Glu	AAC Asn	TAC Tyr	1301
	TTG Leu	CAA Gln	AAA Lys	GAG Glu	GTG Val	GAC Asp	AGT Ser	GGC Gly	CAT His	TGC 430	CCG Cys	CAC Pro	TGG His	GCA Trp	GCC Ala	AGC Ser	1349
60																	

IMMUNEX CORPORATION

Docket No. 2852-A

	CCC	AGC	CCC	AAC	TGG	GCA	GAT	GTC	TGC	ACA	GGC	TGC	CGG	AAC	CCT	CCT	1397
	Pro	Ser	Pro	Asn	Trp	Ala	Asp	Leu	Val	Cys	Thr	Gly	Cys	Arg	Asn	Pro	Pro
			440					445					450				
5	GGG	GAG	GAC	TGT	GAA	CCC	CTC	GTG	GGT	TCC	CCA	AAA	CGT	GGA	CCC	TTG	1445
	Gly	Glu	Asp	Cys	Glu	Pro	Gly	Val	Gly	Ser	Pro	Lys	Arg	Gly	Pro	Leu	
		455					460					465					
10	CCC	CAG	TGC	GCC	TAT	GGC	ATG	GGC	CTT	CCC	CCT	GAA	GAA	GAA	GCC	AGC	1493
	Pro	Gln	Cys	Ala	Tyr	Gly	Met	Gly	Leu	Pro	Pro	Glu	Glu	Glu	Ala	Ser	
		470				475					480					485	
	AGG	ACG	GAG	GCC	AGA	GAC	CAG	CCC	GAG	GAT	GGG	GCT	GAT	GGG	AGG	CTC	1541
15	Arg	Thr	Glu	Ala	Arg	Asp	Gln	Pro	Glu	Asp	Gly	Ala	Asp	Gly	Arg	Leu	
					490					495					500		
	CCA	AGC	TCA	GCG	AGG	GCA	GGT	GCC	GGG	TCT	GGA	AGC	TCC	CCT	GGT	GGC	1589
	Pro	Ser	Ser	Ala	Arg	Ala	Gly	Ala	Gly	Ser	Gly	Ser	Ser	Pro	Gly	Gly	
				505					510					515			
20	CAG	TCC	CCT	GCA	TCT	GGA	AAT	GTG	ACT	GGA	AAC	AGT	AAC	TCC	ACG	TTC	1637
	Gln	Ser	Pro	Ala	Ser	Gly	Asn	Val	Thr	Gly	Asn	Ser	Asn	Ser	Thr	Phe	
			520					525						530			
25	ATC	TCC	AGC	GGG	CAG	GTG	ATG	AAC	TTC	AAG	GGC	GAC	ATC	ATC	GTG	GTC	1685
	Ile	Ser	Ser	Gly	Gln	Val	Met	Asn	Phe	Lys	Gly	Asp	Ile	Ile	Val	Val	
		535					540					545					
30	TAC	GTC	AGC	CAG	ACC	TCG	CAG	GAG	GGC	GCG	GCG	GCT	GCG	GAG	CCC		1733
	Tyr	Val	Ser	Gln	Thr	Ser	Gln	Glu	Gly	Ala	Ala	Ala	Ala	Ala	Glu	Pro	
		550				555					560				565		
	ATG	GGC	CGC	CCG	GTG	CAG	GAG	GAG	ACC	CTG	GCG	CGC	CGA	GAC	TCC	TTC	1781
35	Met	Gly	Arg	Pro	Val	Gln	Glu	Glu	Thr	Leu	Ala	Arg	Arg	Asp	Ser	Phe	
					570					575					580		
	GCG	GGG	AAC	GGC	CCG	CGC	TTC	CCG	GAC	CCG	TGC	GGC	GGC	CCC	GAG	GGG	1829
	Ala	Gly	Asn	Gly	Pro	Arg	Phe	Pro	Asp	Pro	Cys	Gly	Gly	Pro	Glu	Gly	
				585					590					595			
40	CTG	CGG	GAG	CCG	GAG	AAG	GCC	TCG	AGG	CCG	GTG	CAG	GAG	CAA	GGC	GGG	1877
	Leu	Arg	Glu	Pro	Glu	Lys	Ala	Ser	Arg	Pro	Val	Gln	Glu	Gln	Gly	Gly	
			600				605							610			
45	GCC	AAG	GCT	TGAGCGCCCC	CCATGGCTGG	GAGCCCCGAAG	CTCGGAGCCCA										1926
	Ala	Lys	Ala														
		615															
50	GGGCTCGCGA	GGGCAGCACC	GCAGCCTCTG	CCCCAGCCCC	GGCCACCCAG	GGATCGATCG											1986
	GTACAGTCTGA	GGAAGACCAC	CCGGCATTCT	CTGCCCACTT	TGCCTTCCAG	GAATGGGCT											2046
	TTTCAGGAAG	TGAATTGATG	AGGACTGTCC	CCATGCCACC	GGATGCTCAG	CAGCCCCCGG											2106
55	CACTGGGGCA	GATGTCCTCC	CTGCCACTCC	TCAAACCTCGC	AGCAGTAATT	TGTGGCACTA											2166
	TGACAGCTAT	TTTTATGACT	ATCCTGTTCT	GTGGGGGGGG	GGTCTATGTT	TTCCCCCAT											2226
	ATTTGATATC	CTTTTCATAA	CTTTTCTTGA	TATCTTTTCT	CCCTCTTTTT	TAATGTAAAG											2286
60	GTTTTCACAA	AAATTCCTCT	AAAGGTGAGG	GTCTCTTTCT	TTTCTCTTTT	CCTTTTTTTT											2346

TTCTTTT TTTT GGCAACCTGG CTCTGGCCCA GGCTAGAGTG CAGTGGTGGC ATTATAGCCC 2406
 5 GGTGCAGCCT CTAACCTCGT GGCTCAAGCA ATCCAAGTGA TCCTCCCACC TCAACCTTCG 2466
 GAGTAGCTGG GATCACAGCT GCAGGCCACG CCCAGCTTCC TCCCCCGAC TCCCCCCCCC 2526
 CAGAGACACG GTCCCAACCAT GTTACCCAGC CTGGTCTCAA ACTCCCCAGC TAAAGCAGTC 2586
 10 CTCCAGCCTC GGCCTCCCAA AGTACTGGGA TTACAGGCGT GAGCCCCCAC GCTGGCCTGC 2646
 TTACGTATT TTCTTTTGTG CCCCTGCTCA CAGTGTTTTA GAGATGGGCTT TCCCACTGTG 2706
 TGTTCATTGT AAACACTTTT GGGAAAGGGC TAAACATGIG AGGCCTGGAG ATAGTTGCTA 2766
 15 AGTTGCTAGG AACATGTGGT GGGACTTTCA TATTCTGAAA AATGTCTTAT ATTCTCAITT 2826
 TTCTAAAGA AAGAAAAAAG GAAACCCGAT TTATTCTCTC TGAATCTTTT TAAGTTTGTG 2886
 20 TCGTTCCCTTA AGCAGAACTA AGCTCAGTAT GTGACCTTAC CCGCTAGGTG GTTAATTTAT 2946
 CCATGCTGGC AGAGGCACTC AGGTAAGTGG TAAGCAAAAT TCTAAAACTC CAAGTTGCTG 3006
 CAGCTTGCCA TTCTTCTTAT TCTAGAGGTC TCTCTGAAA AGATGGAGAA AATGAACAGG 3066
 25 ACATGGGCT CCTGGAAAGA AAGGGCCCGG GAAGTTC AAG GAAGAATAAA GTTGAAATT 3126
 TAAAAAATAA 3136

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 616 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Pro Arg Ala Arg Arg Arg Pro Leu Phe Ala Leu Leu Leu
 1 5 10 15
 45 Leu Cys Ala Leu Leu Ala Arg Leu Gln Val Ala Leu Gln Ile Ala Pro
 20 25 30
 Pro Cys Thr Ser Glu Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn
 35 40 45
 50 Lys Cys Glu Pro Gly Lys Tyr Met Ser Ser Lys Cys Thr Thr Thr Ser
 50 55 60
 55 Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp
 65 70 75 80
 Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys
 85 90 95
 60 Ala Leu Val Ala Val Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys
 100 105 110

Ala Cys Thr Ala Gly Tyr His Trp Ser Gln Asp Cys Glu Cys Cys Arg
115 120 125

5 Arg Asn Thr Glu Cys Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln
130 135 140

Leu Asn Lys Asp Thr Val Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser
145 150 155 160

10 Asp Ala Phe Ser Ser Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr
165 170 175

Phe Leu Gly Lys Arg Val Glu His His Gly Thr Glu Lys Ser Asp Ala
180 185 190

15 Val Cys Ser Ser Ser Leu Pro Ala Arg Lys Pro Pro Asn Glu Pro His
195 200 205

20 Val Tyr Leu Pro Gly Leu Ile Ile Leu Leu Leu Phe Ala Ser Val Ala
210 215 220

Leu Val Ala Ala Ile Ile Phe Gly Val Cys Tyr Arg Lys Lys Gly Lys
225 230 235 240

25 Ala Leu Thr Ala Asn Leu Trp His Trp Ile Asn Glu Ala Cys Gly Arg
245 250 255

Leu Ser Gly Asp Lys Glu Ser Ser Gly Asp Ser Cys Val Ser Thr His
260 265 270

30 Thr Ala Asn Phe Gly Gln Gln Gly Ala Cys Glu Gly Val Leu Leu Leu
275 280 285

35 Thr Leu Glu Glu Lys Thr Phe Pro Glu Asp Met Cys Tyr Pro Asp Gln
290 295 300

Gly Gly Val Cys Gln Gly Thr Cys Val Gly Gly Gly Pro Tyr Ala Gln
305 310 315 320

40 Gly Glu Asp Ala Arg Met Leu Ser Leu Val Ser Lys Thr Glu Ile Glu
325 330 335

Glu Asp Ser Phe Arg Gln Met Pro Thr Glu Asp Glu Tyr Met Asp Arg
340 345 350

45 Pro Ser Gln Pro Thr Asp Gln Leu Leu Phe Leu Thr Glu Pro Gly Ser
355 360 365

50 Lys Ser Thr Pro Pro Phe Ser Glu Pro Leu Glu Val Gly Glu Asn Asp
370 375 380

Ser Leu Ser Gln Cys Phe Thr Gly Thr Gln Ser Thr Val Gly Ser Glu
385 390 395 400

55 Ser Cys Asn Cys Thr Glu Pro Leu Cys Arg Thr Asp Trp Thr Pro Met
405 410 415

Ser Ser Glu Asn Tyr Leu Gln Lys Glu Val Asp Ser Gly His Cys Pro
420 425 430

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IMMUNEX CORPORATION

Docket No. 2852-A

His Trp Ala Ala Ser Pro Ser Pro Asn Trp Ala Asp Val Cys Thr Gly
 435 440 445
 5 Cys Arg Asn Pro Pro Gly Glu Asp Cys Glu Pro Leu Val Gly Ser Pro
 450 455 460
 Lys Arg Gly Pro Leu Pro Gln Cys Ala Tyr Gly Met Gly Leu Pro Pro
 465 470 475 480
 10 Glu Glu Glu Ala Ser Arg Thr Glu Ala Arg Asp Gln Pro Glu Asp Gly
 485 490 495
 Ala Asp Gly Arg Leu Pro Ser Ser Ala Arg Ala Gly Ala Gly Ser Gly
 500 505 510
 15 Ser Ser Pro Gly Gly Gln Ser Pro Ala Ser Gly Asn Val Thr Gly Asn
 515 520 525
 20 Ser Asn Ser Thr Phe Ile Ser Ser Gly Gln Val Met Asn Phe Lys Gly
 530 535 540
 Asp Ile Ile Val Val Tyr Val Ser Gln Thr Ser Gln Glu Gly Ala Ala
 545 550 555 560
 25 Ala Ala Ala Glu Pro Met Gly Arg Pro Val Gln Glu Glu Thr Leu Ala
 565 570 575
 Arg Arg Asp Ser Phe Ala Gly Asn Gly Pro Arg Phe Pro Asp Pro Cys
 580 585 590
 30 Gly Gly Pro Glu Gly Leu Arg Glu Pro Glu Lys Ala Ser Arg Pro Val
 595 600 605
 35 Gln Glu Gln Gly Gly Ala Lys Ala
 610 615

(2) INFORMATION FOR SEQ ID NO:7:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear
 45
 (ii) MOLECULE TYPE: peptide
 (vii) IMMEDIATE SOURCE:
 (B) CLONE: FLAG® peptide
 50
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asp Tyr Lys Asp Asp Asp Lys
 1 5

55

(2) INFORMATION FOR SEQ ID NO:8:

- 60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 232 amino acids
 (B) TYPE: amino acid

IMMUNEX CORPORATION

Docket No. 2852-A

(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(vii) IMMEDIATE SOURCE:

(B) CLONE: IgG1 Fc mutein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

15	Glu	Pro	Arg	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala
	1				5					10					15	
	Pro	Glu	Ala	Glu	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro
				20					25					30		
20	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val
			35					40					45			
	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val
	50						55					60				
25	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln
	65					70					75				80	
	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln
					85					90				95		
	Asp	Trp	Leu	Asn	Gly	Lys	Asp	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala
			100						105					110		
35	Leu	Pro	Ala	Pro	Met	Gln	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro
			115					120					125			
	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr
	130						135					140				
40	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Arg
	145					150					155				160	
	His	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr
				165					170					175		
	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr
				180					185					190		
50	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe
			195					200					205			
	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys
	210						215					220				
55	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys								
	225					230										

(2) INFORMATION FOR SEQ ID NO:9:

IMMUNEX CORPORATION

Docket No. 2852-A

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: CMV (R2780 Leader)

(ix) FEATURE:
 (D) OTHER INFORMATION: Met1-Arg28 is the actual leader peptide;
 Arg29 strengthens the furin cleavage site; nucleotides
 encoding Thr30 and Ser31 add a Spel site.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Ala	Arg	Arg	Leu	Trp	Ile	Leu	Ser	Leu	Leu	Ala	Val	Thr	Leu	Thr
1				5				10					15		
Val	Ala	Leu	Ala	Ala	Pro	Ser	Gln	Lys	Ser	Lys	Arg	Arg	Thr	Ser	
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1630 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Mus musculus

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY:
 (B) CLONE: RANKL

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 3..884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CC	GGC	GTC	CCA	CAC	GAG	GGT	CCG	CTG	CAC	CCC	GCG	CCT	TCT	GCA	CCG
Gly	Val	Pro	His	Glu	Gly	Pro	Leu	His	Pro	Ala	Pro	Ser	Ala	Pro	
	1			5				10					15		

47

IMMUNEX CORPORATION

Docket No. 2852-A

	GCT	CCG	GCG	CCG	CCA	CCC	GCC	GCC	TCC	CGC	TCC	ATG	TTC	CTG	GCC	CTC	95
	Ala	Pro	Ala	Pro	Pro	Pro	Ala	Ala	Ser	Arg	Ser	Met	Phe	Leu	Ala	Leu	
					20					25					30		
5	CTG	GGG	CTG	GGA	CTG	GGC	CAG	GTG	GTC	TGC	AGC	ATC	GCT	CTG	TTC	CTG	143
	Leu	Gly	Leu	Gly	Leu	Gly	Gln	Val	Val	Cys	Ser	Ile	Ala	Leu	Phe	Leu	
				35					40					45			
10	TAC	TTT	CGA	GCG	CAG	ATG	GAT	CCT	AAC	AGA	ATA	TCA	GAA	GAC	AGC	ACT	191
	Tyr	Phe	Arg	Ala	Gln	Met	Asp	Pro	Asn	Arg	Ile	Ser	Glu	Asp	Ser	Thr	
			50					55					60				
15	CAC	TGC	TTT	TAT	AGA	ATC	CTG	AGA	CTC	CAT	GAA	AAC	GCA	GAT	TTG	CAG	239
	His	Cys	Phe	Tyr	Arg	Ile	Leu	Arg	Leu	His	Glu	Asn	Ala	Asp	Leu	Gln	
		65					70					75					
20	GAC	TCG	ACT	CTG	GAG	AGT	GAA	GAC	ACA	CTA	CCT	GAC	TCC	TGC	AGG	AGG	287
	Asp	Ser	Thr	Leu	Glu	Ser	Glu	Asp	Thr	Leu	Pro	Asp	Ser	Ser	Cys	Arg	
	80					85					90					95	
25	ATG	AAA	CAA	GCC	TTT	CAG	GGG	GCC	GTG	CAG	AAG	GAA	CTG	CAA	CAC	ATT	335
	Met	Lys	Gln	Ala	Phe	Gln	Gly	Ala	Val	Gln	Lys	Glu	Leu	Gln	His	Ile	
				100					105					110			
30	GTG	GGG	CCA	CAG	CGC	TTC	TCA	GGA	GCT	CCA	GCT	ATG	ATG	GAA	Gly	TCA	383
	Val	Gly	Pro	Gln	Arg	Phe	Ser	Gly	Ala	Pro	Ala	Met	Met	Glu	Gly	Ser	
				115					120					125			
35	TGG	TTG	GAT	GTG	GCC	CAG	CGA	GGC	AAG	CCT	GAG	GCC	CAG	CCA	TTT	GCA	431
	Trp	Leu	Asp	Val	Ala	Gln	Arg	Gly	Lys	Pro	Glu	Ala	Gln	Pro	Phe	Ala	
			130					135					140				
40	CAC	CTC	ACC	ATC	AAT	GCT	GCC	AGC	ATC	CCA	TCG	GGT	TCC	CAT	AAA	GTC	479
	His	Leu	Thr	Ile	Asn	Ala	Ala	Ser	Ile	Pro	Ser	Gly	Ser	His	Lys	Val	
		145					150					155					
45	ACT	CTG	TCC	TCT	TGG	TAC	CAC	GAT	CGA	GGC	TGG	GCC	AAG	ATC	TCT	AAC	527
	Thr	Leu	Ser	Ser	Trp	Tyr	His	Asp	Arg	Gly	Trp	Ala	Lys	Ile	Ser	Asn	
	160					165					170					175	
50	ATG	ACG	TTA	AGC	AAC	GGA	AAA	CTA	AGG	GTT	AAC	CAA	GAT	GGC	TTC	TAT	575
	Met	Thr	Leu	Ser	Asn	Gly	Lys	Leu	Arg	Val	Asn	Gln	Asp	Gly	Phe	Tyr	
					180				185							190	
55	TAC	CTG	TAC	GCC	AAC	ATT	TGC	TTT	CGG	CAT	CAT	GAA	ACA	TCG	GGA	AGC	623
	Tyr	Leu	Tyr	Ala	Asn	Ile	Cys	Phe	Arg	His	His	Glu	Thr	Ser	Gly	Ser	
				195					200					205			
60	GTA	CCT	ACA	GAC	TAT	CTT	CAG	CTG	ATG	GTG	TAT	GTC	GTT	AAA	ACC	AGC	671
	Val	Pro	Thr	Asp	Tyr	Leu	Gln	Leu	Met	Val	Tyr	Val	Val	Lys	Thr	Ser	
			210					215					220				
65	ATC	AAA	ATC	CCA	AGT	TCT	CAT	AAC	CTG	ATG	AAA	GGA	GGG	AGC	ACG	AAA	719
	Ile	Lys	Ile	Pro	Ser	Ser	His	Asn	Leu	Met	Lys	Gly	Gly	Ser	Thr	Lys	
		225					230					235					
70	AAC	TGG	TCG	GGC	AAT	TCT	GAA	TTC	CAC	TTT	TAT	TCC	ATA	AAT	GTT	GGG	767
	Asn	Trp	Ser	Gly	Asn	Ser	Glu	Phe	His	Phe	Tyr	Ser	Ile	Asn	Val	Gly	
	240					245					250					255	

IMMUNEX CORPORATION

Docket No. 2852-A

Cys Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Asp Leu Gln Asp
 65 70 75 80
 5 Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met
 85 90 95
 Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val
 100 105 110
 10 Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp
 115 120 125
 Leu Asp Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His
 130 135 140
 15 Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr
 145 150 155 160
 20 Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met
 165 170 175
 Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr
 180 185 190
 25 Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val
 195 200 205
 Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile
 210 215 220
 30 Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn
 225 230 235 240
 35 Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly
 245 250 255
 Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn
 260 265 270
 40 Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe
 275 280 285
 Lys Val Gln Asp Ile Asp
 290

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 954 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 50
 55 (ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 60 (vi) ORIGINAL SOURCE:

IMMUNEX CORPORATION

Docket No. 2852-A

(A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:

5 (B) CLONE: huRANKL (full length)

(ix) FEATURE:

(A) NAME/KEY: CDS

10 (B) LOCATION: 1..951

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

15	ATG CGC CGC GCC AGC AGA GAC TAC ACC AAG TAC CTG CGT GGC TCG GAG	48
	Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser Glu	
	1 5 10 15	
20	GAG ATG GGC GGC GGC CCC GGA GCC CCG CAC GAG GGC CCC CTG CAC GCC	96
	Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His Ala	
	20 25 30	
25	CCG CCG CCG CCT GCG CCG CAC CAG CCC CCC GCC GCC TCC CGC TCC ATG	144
	Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser Met	
	35 40 45	
30	TTC GTG GCC CTC CTG GGG CTG GGG CTG GGC CAG GTT GTC TGC AGC GTC	192
	Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Val	
	50 55 60	
35	GCC CTG TTC TTC TAT TTC AGA GCG CAG ATG GAT CCT AAT AGA ATA TCA	240
	Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser	
	65 70 75 80	
40	GAA GAT GGC ACT CAC TGC ATT TAT AGA ATT TTG AGA CTC CAT GAA AAT	288
	Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn	
	85 90 95	
45	GCA GAT TTT CAA GAC ACA ACT CTG GAG AGT CAA GAT ACA AAA TTA ATA	336
	Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile	
	100 105 110	
50	CCT GAT TCA TGT AGG AGA ATT AAA CAG GCC TTT CAA GGA GCT GTG CAA	384
	Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln	
	115 120 125	
55	AAG GAA TTA CAA CAT ATC GTT GGA TCA CAG CAC ATC AGA GCA GAG AAA	432
	Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys	
	130 135 140	
60	GCG ATG GTG GAT GGC TCA TGG TTA GAT CTG GCC AAG AGG AGC AAG CTT	480
	Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu	
	145 150 155 160	
65	GAA GCT CAG CCT TTT GCT CAT CTC ACT ATT AAT GCC ACC GAC ATC CCA	528
	Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro	
	165 170 175	
70	TCT GGT TCC CAT AAA GTG AGT CTG TCC TCT TGG TAC CAT GAT CGG GGT	576
	Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly	
	180 185 190	

IMMUNEX CORPORATION

Docket No. 2852-A

	TGG	GCC	AAG	ATC	TCC	AAC	ATG	ACT	TTT	AGC	AAT	GGA	AAA	CTA	ATA	GTT	624
	Trp	Ala	Lys	Ile	Ser	Asn	Met	Thr	Phe	Ser	Asn	Gly	Lys	Leu	Ile	Val	
			195					200					205				
5	AAT	CAG	GAT	GGC	TTT	TAT	TAC	CTG	TAT	GCC	AAC	ATT	TGC	TTT	CGA	CAT	672
	Asn	Gln	Asp	Gly	Phe	Tyr	Tyr	Leu	Tyr	Ala	Asn	Ile	Cys	Phe	Arg	His	
			210				215					220					
10	CAT	GAA	ACT	TCA	GGA	GAC	CTA	GCT	ACA	GAG	TAT	CTT	CAA	CTA	ATG	GTG	720
	His	Glu	Thr	Ser	Gly	Asp	Leu	Ala	Thr	Glu	Tyr	Leu	Gln	Leu	Met	Val	
			225			230					235					240	
15	TAC	GTC	ACT	AAA	ACC	AGC	ATC	AAA	ATC	CCA	AGT	TCT	CAT	ACC	CTG	ATG	768
	Tyr	Val	Thr	Lys	Thr	Ser	Ile	Lys	Ile	Pro	Ser	Ser	His	Thr	Leu	Met	
					245					250					255		
20	AAA	GGA	GGA	AGC	ACC	AAG	TAT	TGG	TCA	GGG	AAT	TCT	GAA	TTC	CAT	TTT	816
	Lys	Gly	Gly	Ser	Thr	Lys	Tyr	Trp	Ser	Gly	Asn	Ser	Glu	Phe	His	Phe	
				260					265					270			
25	TAT	TCC	ATA	AAC	GTT	GGT	GGA	TTT	TTT	AAG	TTA	CGG	TCT	GGA	GAG	GAA	864
	Tyr	Ser	Ile	Asn	Val	Gly	Gly	Phe	Phe	Lys	Leu	Arg	Ser	Gly	Glu	Glu	
				275			280						285				
30	ATC	AGC	ATC	GAG	GTC	TCC	AAC	CCC	TCC	TTA	CTG	GAT	CCG	GAT	CAG	GAT	912
	Ile	Ser	Ile	Glu	Val	Ser	Asn	Pro	Ser	Leu	Leu	Asp	Pro	Asp	Gln	Asp	
				290			295			300							
35	GCA	ACA	TAC	TTT	GGG	GCT	TTT	AAA	GTT	CGA	GAT	ATA	GAT	TGA			954
	Ala	Thr	Tyr	Phe	Gly	Ala	Phe	Lys	Val	Arg	Asp	Ile	Asp				
				305			310				315						
	(2) INFORMATION FOR SEQ ID NO:13:																
40	(i) SEQUENCE CHARACTERISTICS:																
	(A) LENGTH: 317 amino acids																
	(B) TYPE: amino acid																
	(D) TOPOLOGY: linear																
	(ii) MOLECULE TYPE: protein																
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:																
45	Met	Arg	Arg	Ala	Ser	Arg	Asp	Tyr	Thr	Lys	Tyr	Leu	Arg	Gly	Ser	Glu	
	1				5					10					15		
	Glu	Met	Gly	Gly	Gly	Pro	Gly	Ala	Pro	His	Glu	Gly	Pro	Leu	His	Ala	
				20					25					30			
50	Pro	Pro	Pro	Pro	Ala	Pro	His	Gln	Pro	Pro	Ala	Ala	Ser	Arg	Ser	Met	
				35				40					45				
55	Phe	Val	Ala	Leu	Leu	Gly	Leu	Gly	Leu	Gly	Gln	Val	Val	Cys	Ser	Val	
		50					55					60					
	Ala	Leu	Phe	Phe	Tyr	Phe	Arg	Ala	Gln	Met	Asp	Pro	Asn	Arg	Ile	Ser	
		65				70				75					80		
60	Glu	Asp	Gly	Thr	His	Cys	Ile	Tyr	Arg	Ile	Leu	Arg	Leu	His	Glu	Asn	
					85					90					95		

Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile
 100 105 110

5 Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln
 115 120 125

Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys
 130 135 140

10 Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu
 145 150 155 160

Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro
 165 175

15 Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly
 180 185 190

20 Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val
 195 200 205

Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
 210 215 220

25 His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val
 225 230 235 240

Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met
 245 255

Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe
 260 265 270

35 Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu
 275 280 285

Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
 290 295 300

40 Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp
 305 310 315

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1878 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Murine

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Murine Fetal Liver Epithelium

(B) CLONE: muRANK

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

5	ATG GCC CCG CGC GCC CGG CGG CGC CGC CAG CTG CCC GCG CCG CTG CTG	48
15	Met Ala Pro Arg Ala Arg Arg Arg Arg Gln Leu Pro Ala Pro Leu Leu	
	1 5 10 15	
20	GCG CTC TGC GTG CTG CTC GTT CCA CTG CAG GTG ACT CTC CAG GTC ACT	96
	Ala Leu Cys Val Leu Leu Val Pro Leu Gln Val Thr Leu Val Thr	
	20 25 30	
25	CCT CCA TGC ACC CAG GAG AGG CAT TAT GAG CAT CTC GGA CCG TGT TGC	144
	Pro Pro Cys Thr Gln Glu Arg His Tyr Glu His Leu Gly Arg Cys Cys	
	35 40 45	
30	AGC AGA TGC GAA CCA GGA AAG TAC CTG TCC TCT AAG TGC ACT CCT ACC	192
	Ser Arg Cys Glu Pro Gly Lys Tyr Leu Ser Ser Lys Cys Thr Pro Thr	
	50 55 60	
35	TCC GAC AGT GTG TGT CTG CCC TGT GGC CCC GAT GAG TAC TTG GAC ACC	240
	Ser Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Thr	
	65 70 75 80	
40	TGG AAT GAA GAA GAT AAA TGC TTG CTG CAT AAA GTC TGT GAT GCA GGC	288
	Trp Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Ala Gly	
	85 90 95	
45	AAG GCC CTG GTG GCG GTG GAT CCT GGC AAC CAC ACG GCC CCG CGT CGC	336
	Lys Ala Leu Val Ala Val Asp Pro Gly Asn His Thr Ala Pro Arg Arg	
	100 105 110	
50	TGT GCT TGC ACG GCT GGC TAC CAC TGG AAC TCA GAC TGC GAG TGC TGC	384
	Cys Ala Cys Thr Ala Gly Tyr His Trp Asn Ser Asp Cys Glu Cys Cys	
	115 120 125	
55	CGC AGG AAC ACG GAG TGT GCA CCT GGC TTC GGA GCT CAG CAT CCC TTG	432
	Arg Arg Asn Thr Glu Cys Ala Pro Gly Phe Gly Ala Gln His Pro Leu	
	130 135 140	
60	CAG CTC AAC AAG GAT ACG GTG TGC ACA CCC TGC CTC CTG GGC TTC TTC	480
	Gln Leu Asn Lys Asp Thr Val Cys Thr Pro Cys Leu Leu Gly Phe Phe	
	145 150 155 160	
	TCA GAT GTC TTT TCG TCC ACA GAC AAA TGC AAA CCT TGG ACC AAC TGC	528
	Ser Asp Val Phe Ser Ser Thr Asp Lys Cys Lys Pro Trp Thr Asn Cys	
	165 170 175	
	ACC CTC CTT GGA AAG CTA GAA GCA CAC CAG GGG ACA ACG GAA TCA GAT	576
	Thr Leu Leu Gly Lys Leu Glu Ala His Gln Gly Thr Thr Glu Ser Asp	
	180 185 190	

IMMUNEX CORPORATION

Docket No. 2852-A

	GTG	GTC	TGC	AGC	TCT	TCC	ATG	ACA	CTG	AGG	AGA	CCA	CCC	AAG	GAG	GCC	624
	Val	Val	Cys	Ser	Ser	Ser	Met	Thr	Leu	Arg	Arg	Pro	Pro	Lys	Glu	Ala	
			195					200					205				
5	CAG	GCT	TAC	CTG	CCC	AGT	CTC	ATC	GTT	CTG	CTC	CTC	TTC	ATC	TCT	GTG	672
	Gln	Ala	Tyr	Leu	Pro	Ser	Leu	Ile	Val	Leu	Leu	Leu	Phe	Ile	Ser	Val	
		210					215					220					
10	GTA	GTA	GTG	GCT	GCC	ATC	ATC	TTC	GGC	GTT	TAC	TAC	AGG	AAG	GGA	GGG	720
	Val	Val	Val	Ala	Ala	Ile	Ile	Phe	Gly	Val	Tyr	Tyr	Arg	Lys	Gly	Gly	
		225				230					235				240		
15	AAA	CGC	CTG	ACA	GCT	AAT	TTG	TGG	AAT	TGG	GTC	AAT	GAT	GCT	TGC	AGT	768
	Lys	Ala	Leu	Thr		Asn	Leu	Trp	Asn		Val	Asn	Asp	Ala	Cys	Ser	
					245					250					255		
20	AGT	CTA	AGT	GGA	AAT	AAG	GAG	TCC	TCA	GGG	GAC	CGT	TGT	GCT	GGT	TCC	816
	Ser	Leu	Ser	Gly	Asn	Lys	Glu	Ser	Ser	Gly	Asp	Arg	Cys	Ala	Gly	Ser	
					260				265					270			
25	CAC	TCG	GCA	ACC	TCC	AGT	CAG	CAA	GAA	GTG	TGT	GAA	GGT	ATC	TTA	CTA	864
	His	Ser	Ala	Thr	Ser	Ser	Gln	Gln	Glu	Val	Cys	Glu	Gly	Ile	Leu	Leu	
			275					280					285				
30	ATG	ACT	CGG	GAG	GAG	AAG	ATG	GTT	CCA	GAA	GAC	GGT	GCT	GGA	GTC	TGT	912
	Met	Thr	Arg	Glu	Glu	Lys	Met	Val	Pro	Glu	Asp	Gly	Ala	Gly	Val	Cys	
			290				295					300					
35	GGG	CCT	GTG	TGT	GCG	GCA	GGT	GGG	CCC	TGG	GCA	GAA	GTC	AGA	GAT	TCT	960
	Gly	Pro	Val	Cys	Ala	Ala	Gly	Gly	Pro	Trp	Ala	Glu	Val	Arg	Asp	Ser	
		305				310					315				320		
40	AGG	ACG	TTC	ACA	CTG	GTC	AGC	GAG	GTT	GAG	ACG	CAA	GGA	GAC	CTC	TCG	1008
	Arg	Thr	Phe	Thr	Leu	Val	Ser	Glu	Val	Glu	Thr	Gln	Gly	Asp	Leu	Ser	
					325					330					335		
45	AGG	AAG	ATT	CCC	ACA	GAG	GAT	GAG	TAC	ACG	GAC	CGG	CCC	TCG	CAG	CCT	1056
	Arg	Lys	Ile	Pro	Thr	Glu	Asp	Glu	Tyr	Thr	Asp	Arg	Pro	Ser	Gln	Pro	
				340					345					350			
50	TCG	ACT	GGT	TCA	CTG	CTC	CTA	ATC	CAG	CAG	GGA	AGC	AAA	TCT	ATA	CCC	1104
	Ser	Thr	Gly	Ser	Leu	Leu	Leu	Ile	Gln	Gln	Gly	Ser	Lys	Ser	Ile	Pro	
			355					360					365				
55	CCA	TTC	CAG	GAG	CCC	CTG	GAA	GTG	GGG	GAG	AAC	GAC	AGT	TTA	AGC	CAG	1152
	Pro	Phe	Gln	Glu	Pro	Leu	Val	Gly	Glu	Asn	Asp	Ser	Ser	Leu	Ser	Gln	
			370				375					380					
60	TGT	TTC	ACC	GGG	ACT	GAA	AGC	ACG	GTG	GAT	TCT	GAG	GGC	TGT	GAC	TTC	1200
	Cys	Phe	Thr	Gly	Thr	Glu	Ser	Thr	Val	Asp	Ser	Glu	Gly	Cys	Asp	Phe	
		385				390					395				400		
65	ACT	GAG	CCT	CCG	AGC	AGA	ACT	GAC	TCT	ATG	CCC	GTG	TCC	CCT	GAA	AAG	1248
	Thr	Glu	Pro	Pro	Ser	Arg	Thr	Asp	Ser	Met	Pro	Val	Ser	Pro	Glu	Lys	
					405					410					415		
70	CAC	CTG	ACA	AAA	GAA	ATA	GAA	GGT	GAC	AGT	TGC	CTC	CCC	TGG	GTG	GTC	1296
	His	Leu	Thr	Lys	Glu	Ile	Glu	Gly	Asp	Ser	Cys	Leu	Pro	Trp	Val	Val	
					420				425					430			

IMMUNEX CORPORATION

Docket No. 2852-A

	AGC	TCC	AAC	TCA	ACA	GAT	GGC	TAC	ACA	GGC	AGT	GGG	AAC	ACT	CCT	GGG	1344
	Ser	Ser	Asn	Ser	Thr	Asp	Gly	Tyr	Thr	Gly	Ser	Gly	Asn	Thr	Pro	Gly	
			435					440					445				
5	GAG	GAC	CAT	GAA	CCC	TTT	CCA	GGG	TCC	CTG	AAA	TGT	GGA	CCA	TTG	CCC	1392
	Glu	Asp	His	Glu	Pro	Phe	Pro	Gly	Ser	Leu	Lys	Cys	Gly	Pro	Leu	Pro	
		450					455				460						
10	CAG	TGT	GCC	TAC	AGC	ATG	GGC	TTT	CCC	AGT	GAA	GCA	GCA	GCC	AGC	ATG	1440
	Gln	Cys	Ala	Tyr	Ser	Met	Gly	Phe	Pro	Ser	Glu	Ala	Ala	Ala	Ser	Met	
		465				470					475				480		
	GCA	GAG	GCG	GGA	GTA	CGG	CCC	CAG	GAC	AGG	GCT	GAT	GAG	AGG	GGA	GCC	1488
	Ala	Glu	Ala	Gly	Val	Arg	Pro	Gln	Asp	Arg	Ala	Asp	Glu	Arg	Gly	Ala	
15					485					490					495		
	TCA	GGG	TCC	GGG	AGC	TCC	CCC	AGT	GAC	CAG	CCA	CCT	GCC	TCT	GGG	AAC	1536
	Ser	Gly	Ser	Gly	Ser	Ser	Pro	Ser	Asp	Gln	Pro	Pro	Ala	Ser	Gly	Asn	
				500					505					510			
20	GTG	ACT	GGA	AAC	AGT	AAC	TCC	ACG	TTC	ATC	TCT	AGC	GGG	CAG	GTG	ATG	1584
	Val	Thr	Gly	Asn	Ser	Asn	Ser	Thr	Phe	Ile	Ser	Ser	Gly	Gln	Val	Met	
			515					520					525				
25	AAC	TTC	AAG	GGT	GAC	ATC	ATC	GTG	GTG	TAT	GTG	AGC	CAG	ACC	TCG	CAG	1632
	Asn	Phe	Lys	Gly	Asp	Ile	Ile	Val	Val	Tyr	Val	Ser	Gln	Thr	Ser	Gln	
			530				535					540					
30	GAG	GGC	CCG	GGT	TCC	GCA	GAG	CCC	GAG	TCG	GAG	CCC	GTG	GGC	CGC	CCT	1680
	Glu	Gly	Pro	Gly	Ser	Ala	Glu	Pro	Glu	Ser	Glu	Pro	Val	Gly	Arg	Pro	
		545				550					555					560	
	GTG	CAG	GAG	GAG	ACG	CTG	GCA	CAC	AGA	GAC	TCC	TTT	GCG	GGC	ACC	GCG	1728
	Val	Gln	Glu	Glu	Thr	Leu	Ala	His	Arg	Asp	Ser	Phe	Ala	Gly	Thr	Ala	
35					565					570					575		
	CCG	CGC	TTC	CCC	GAC	GTC	TGT	GCC	ACC	GGG	GCT	GGG	CTG	CAG	GAG	CAG	1776
	Pro	Arg	Phe	Pro	Asp	Val	Cys	Ala	Thr	Gly	Ala	Gly	Leu	Gln	Glu	Gln	
				580					585					590			
40	GGG	GCA	CCC	CGG	CAG	AAG	GAC	GGG	ACA	TCG	CGG	CCG	GTG	CAG	GAG	CAG	1824
	Gly	Ala	Pro	Arg	Gln	Lys	Asp	Gly	Thr	Ser	Arg	Pro	Val	Gln	Glu	Gln	
				595				600					605				
45	GGT	GGG	GCG	CAG	ACT	TCA	CTC	CAT	ACC	CAG	GGG	TCC	GGA	CAA	TGT	GCA	1872
	Gly	Gly	Ala	Gln	Thr	Ser	Leu	His	Thr	Gln	Gly	Ser	Gly	Gln	Cys	Ala	
			610				615					620					
50	GAA	TGA															1878
	Glu																
		625															

(2) INFORMATION FOR SEQ ID NO:15:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 625 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

5 Met Ala Pro Arg Ala Arg Arg Arg Arg Gln Leu Pro Ala Pro Leu Leu
 1 5 10 15
 Ala Leu Cys Val Leu Leu Val Pro Leu Gln Val Thr Leu Gln Val Thr
 20 25 30
 10 Pro Pro Cys Thr Gln Glu Arg His Tyr Glu His Leu Gly Arg Cys Cys
 35 40 45
 Ser Arg Cys Glu Pro Gly Lys Tyr Leu Ser Ser Lys Cys Thr Pro Thr
 50 55 60
 15 Ser Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Thr
 65 70 75 80
 20 Trp Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Ala Gly
 85 90 95
 Lys Ala Leu Val Ala Val Asp Pro Gly Asn His Thr Ala Pro Arg Arg
 100 105 110
 25 Cys Ala Cys Thr Ala Gly Tyr His Trp Asn Ser Asp Cys Glu Cys Cys
 115 120 125
 Arg Arg Asn Thr Glu Cys Ala Pro Gly Phe Gly Ala Gln His Pro Leu
 130 135 140
 30 Gln Leu Asn Lys Asp Thr Val Cys Thr Pro Cys Leu Leu Gly Phe Phe
 145 150 155 160
 35 Ser Asp Val Phe Ser Ser Thr Asp Lys Cys Lys Pro Trp Thr Asn Cys
 165 170 175
 Thr Leu Leu Gly Lys Leu Glu Ala His Gln Gly Thr Thr Glu Ser Asp
 180 185 190
 40 Val Val Cys Ser Ser Ser Met Thr Leu Arg Arg Pro Pro Lys Glu Ala
 195 200 205
 Gln Ala Tyr Leu Pro Ser Leu Ile Val Leu Leu Leu Phe Ile Ser Val
 210 215 220
 45 Val Val Val Ala Ala Ile Ile Phe Gly Val Tyr Arg Lys Gly Gly
 225 230 235 240
 50 Lys Ala Leu Thr Ala Asn Leu Trp Asn Trp Val Asn Asp Ala Cys Ser
 245 250 255
 Ser Leu Ser Gly Asn Lys Glu Ser Ser Gly Asp Arg Cys Ala Gly Ser
 260 265 270
 55 His Ser Ala Thr Ser Ser Gln Gln Glu Val Cys Glu Gly Ile Leu Leu
 275 280 285
 Met Thr Arg Glu Glu Lys Met Val Pro Glu Asp Gly Ala Gly Val Cys
 290 295 300
 60

IMMUNEX CORPORATION

Docket No. 2852-A

Gly Pro Val Cys Ala Ala Gly Gly Pro Trp Ala Glu Val Arg Asp Ser
 305 310 315 320
 5 Arg Thr Phe Thr Leu Val Ser Glu Val Glu Thr Gln Gly Asp Leu Ser
 325 330 335
 Arg Lys Ile Pro Thr Glu Asp Glu Tyr Thr Asp Arg Pro Ser Gln Pro
 340 345 350
 10 Ser Thr Gly Ser Leu Leu Leu Ile Gln Gln Gly Ser Lys Ser Ile Pro
 355 360 365
 Pro Phe Gln Glu Pro Leu Glu Val Gly Glu Asn Asp Ser Leu Ser Gln
 370 375 380
 15 Cys Phe Thr Gly Thr Glu Ser Thr Val Asp Ser Glu Gly Cys Asp Phe
 385 390 395 400
 Thr Glu Pro Pro Ser Arg Thr Asp Ser Met Pro Val Ser Pro Glu Lys
 405 410 415
 20 His Leu Thr Lys Glu Ile Glu Gly Asp Ser Cys Leu Pro Trp Val Val
 420 425 430
 25 Ser Ser Asn Ser Thr Asp Gly Tyr Thr Gly Ser Gly Asn Thr Pro Gly
 435 440 445
 Glu Asp His Glu Pro Phe Pro Gly Ser Leu Lys Cys Gly Pro Leu Pro
 450 455 460
 30 Gln Cys Ala Tyr Ser Met Gly Phe Pro Ser Glu Ala Ala Ala Ser Met
 465 470 475 480
 Ala Glu Ala Gly Val Arg Pro Gln Asp Arg Ala Asp Glu Arg Gly Ala
 485 490 495
 35 Ser Gly Ser Gly Ser Ser Pro Ser Asp Gln Pro Pro Ala Ser Gly Asn
 500 505 510
 40 Val Thr Gly Asn Ser Asn Ser Thr Phe Ile Ser Ser Gly Gln Val Met
 515 520 525
 Asn Phe Lys Gly Asp Ile Ile Val Val Tyr Val Ser Gln Thr Ser Gln
 530 535 540
 45 Glu Gly Pro Gly Ser Ala Glu Pro Glu Ser Glu Pro Val Gly Arg Pro
 545 550 555 560
 Val Gln Glu Glu Thr Leu Ala His Arg Asp Ser Phe Ala Gly Thr Ala
 565 570 575
 50 Pro Arg Phe Pro Asp Val Cys Ala Thr Gly Ala Gly Leu Gln Glu Gln
 580 585 590
 55 Gly Ala Pro Arg Gln Lys Asp Gly Thr Ser Arg Pro Val Gln Glu Gln
 595 600 605
 Gly Gly Ala Gln Thr Ser Leu His Thr Gln Gly Ser Gly Gln Cys Ala
 610 615 620
 60

IMMUNEX CORPORATION

Docket No. 2852-A

Glu
625

5 (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

15

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

20

Gly Ser Thr Gly
20

25

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

35

Asp Tyr Lys Asp Glu
5

40

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

50

His His His His His
5

55

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

60

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

5 Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile
1 5 10 15
Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu
20 25 30
10 Arg

15